

## RESULT 6

## HUMIRGT

LOCUS HUMIRGT 2128 bp mRNA linear PRI 06-JAN-1995

DEFINITION Human insulin-responsive glucose transporter (GLUT4) mRNA, complete cds.

ACCESSION M20747

VERSION M20747.1 GI:186552

KEYWORDS insulin-responsive glucose transporter.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2128)

AUTHORS Fukumoto,H., Kayano,T., Buse,J.B., Edwards,Y., Pilch,P.F., Bell,G.I. and Seino,S.

TITLE Cloning and characterization of the major insulin-responsive glucose transporter expressed in human skeletal muscle and other insulin-responsive tissues

JOURNAL J. Biol. Chem. 264 (14), 7776-7779 (1989)

PUBMED 2656669

COMMENT Original source text: Human jejunum and muscle, cDNA to mRNA, clones lambda-h-[JHT-3, AMT-6, FMT-1].  
Draft entry and computer-readable sequence for [1] kindly provided by G.I.Bell, 19-APR-1989.

## FEATURES

source Location/Qualifiers

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CDS

146..1675  
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/db\_xref="GI:307076"  
/db\_xref="GDB:G00-119-997"  
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SQWLGRKRAMLVNNVLAVLGGSLMGLANAAASYEMLIIGRFLIGAYSGLTSLVPMYV  
GEIAPTHLRGALGTLNQLAIVIGILIAQVLGLESLLGTASLWPLLLGLTVLPALLQLV  
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## ORIGIN

Query Match 99.9%; Score 1528.4; DB 8; Length 2128;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1529; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 206 ACTGGGACCTGGTCCTTGCTGTGTTCTCTGCGGTGCTTGGCTCCCTGCAGTTTGGGTAC 265

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Qy 181 CTGGGGAGGCAGGGGCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCCTCACCACCCCTC 240  
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QY      1081 TGTGGCTGTGCCATCCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATG 1140
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Db      1226 TGTGGCTGTGCCATCCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATG 1285
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Db      1406 GCTGTGGCTGGTTTCTCCAAGTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTAT 1465
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Query Match 99.8%; Score 1526.8; DB 14; Length 2128;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1528; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

http://es/ScoreAccessWeb/GetItem.action?AppId=10659234&seqId=505575&ItemName=us-... 6/5/06

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Qy	301	ATCATCTCTCAGTGGCTTGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTG	360
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Qy	481	GGGGAGATTGCTCCCACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATT	540
Db	626	GGGGAGATTGCTCCCACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATT	685
Qy	541	GTTATCGGCATTCTGATCGCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGC	600
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Qy	601	CTGTGGCCACTGCTCCTGGGCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGCTG	660
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Qy	661	CCCTTCTGTCCCAGAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCC	720
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Met → val

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Db      1466 GTTGC GGAGGCTATGGGGCCCTACGCTTCCTTCTATTTGCGGTCTCCTGCTGGGCTTC 1525
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RESULT 1  
US-09-591-025-8  
; Sequence 8, Application US/09591025  
; Patent No. 6303373  
; GENERAL INFORMATION:  
; APPLICANT: Bogan, Jonathan S.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: Method of Measuring Plasma Membrane  
; TITLE OF INVENTION: Targeting of GLUT4  
; FILE REFERENCE: 0399.1210-004  
; CURRENT APPLICATION NUMBER: US/09/591,025  
; CURRENT FILING DATE: 2000-06-09  
; PRIOR APPLICATION NUMBER: 60/154,078  
; PRIOR FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/138,237  
; PRIOR FILING DATE: 1999-06-09  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 2592  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: modified GLUT4 containing myc tag sequences  
US-09-591-025-8

Query Match 86.6%; Score 1325; DB 3; Length 2592;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1328; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

*Low Score*

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Qy	255	GGCCATCTTTCCGTGGGCGGCATGATTTCTCCTCCTCATTGGTATCATCTCTCAGTG	314
Db	570	GGCCATCTTTCCGTGGGCGGCATGATTTCTCCTCCTCATTGGTATCATCTCTCAGTG	629
Qy	315	GCTTGGAAGGAAAAGGCCATGCTGGTCAACAATGTCTGGCGGTGCTGGGGGGCAGCCT	374
Db	630	GCTTGGAAGGAAAAGGCCATGCTGGTCAACAATGTCTGGCGGTGCTGGGGGGCAGCCT	689
Qy	375	CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCTCAT	434
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Db	810	CACTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTATCGGCATTCT	869
Qy	555	GATCGCCAGGTGCTGGGCTTGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT	614
Db	870	GATCGCCAGGTGCTGGGCTTGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT	929
Qy	615	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGCTGCCCTTCTGTCCCGA	674
Db	930	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGCTGCCCTTCTGTCCCGA	989
Qy	675	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	734
Db	990	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	1049
Qy	735	GCGCCTGACAGGCTGGGCGCATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	794
Db	1050	GCGCCTGACAGGCTGGGCGCATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	1109
Qy	795	GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG	854
Db	1110	GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG	1169
Qy	855	GCAGCCCCCTGATCATTGCGGTGCTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	914
Db	1170	GCAGCCCCCTGATCATTGCGGTGCTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	1229
Qy	915	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	974
Db	1230	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	1289

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Qy      975 CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA 1034
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Qy      1035 GCGGGCGGGGCGCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1094
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Db      1350 GCGGGCGGGGCGCGGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT 1409

Qy      1095 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1154
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Db      1410 CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATGAGCTACGTCTCCAT 1469

Qy      1155 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGGAGATTGGCCCTGGCCCCATTCTTGGTT 1214
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Db      1470 TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGGAGATTGGCCCTGGCCCCATTCTTGGTT 1529

Qy      1215 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT 1274
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Db      1530 CATCGTGGCCGAGCTCTTCAGCCAGGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT 1589

Qy      1275 CTCCAACCTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1334
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Db      1590 CTCCAACCTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT 1649

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Qy      1395 CTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCAGCTGCCTTCCACCG 1454
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Db      1710 CTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCGGCTGCCTTCCACCG 1769

Qy      1455 GACACCCTCTCTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1514
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## RESULT 2

US-09-894-927B-8

; Sequence 8, Application US/09894927B

; Patent No. 6632924

; GENERAL INFORMATION:

; APPLICANT: Bogan, Jonathan S.

; APPLICANT: Lodish, Harvey F.

; TITLE OF INVENTION: Method of Measuring Plasma Membrane

; TITLE OF INVENTION: Targeting of GLUT4

; FILE REFERENCE: 0399.1210-005

; CURRENT APPLICATION NUMBER: US/09/894,927B

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/591,025

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: US 60/154,078

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: US 60/138,237

; PRIOR FILING DATE: 1999-06-09

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 2592

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: modified GLUT4 containing myc tag sequences

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2592)

US-09-894-927B-8

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Query Match      86.4%; Score 1321.8; DB 3; Length 2592;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1326; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Qy      195 GCCTGAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCAT 254
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Db      510 GCTTAAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCGT 569
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Qy	255	GGCCATCTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGTATCATCTCTCAGTG	314
Db	570	GGCCATCTTTCCGTGGGCGGCATGATTTCCTCCTTCCTCATTGGTATCATCTCTCAGTG	629
Qy	315	GCTTGAAGGAAAAGGGCCATGCTGGTCAACAATGTCTGGCGGTGCTGGGGGCGAGCCT	374
Db	630	GCTTGAAGGAAAAGGGCCATGCTGGTCAACAATGTCTGGCGGTGCTGGGGGCGAGCCT	689
Qy	375	CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCTCAT	434
Db	690	CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCTCAT	749
Qy	435	TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC	494
Db	750	TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC	809
Qy	495	CACCTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT	554
Db	810	CACCTCACCTGCGGGGCGCCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT	869
Qy	555	GATCGCCAGGTGCTGGGCTTGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT	614
Db	870	GATCGCCAGGTGCTGGGCTTGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT	929
Qy	615	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGCTGCCCTTCTGTCCCGA	674
Db	930	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGCTGCCCTTCTGTCCCGA	989
Qy	675	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	734
Db	990	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	1049
Qy	735	GCGCCTGACAGGTGGGCGGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	794
Db	1050	GCGCCTGACAGGTGGGCGGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	1109
Qy	795	GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG	854
Db	1110	GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG	1169
Qy	855	GCAGCCCCGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	914
Db	1170	GCAGCCCCGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	1229
Qy	915	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	974
Db	1230	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	1289
Qy	975	CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA	1034
Db	1290	CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA	1349
Qy	1035	GCGGGCGGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT	1094
Db	1350	GCGGGCGGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT	1409
Qy	1095	CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCAGCCATGAGCTACGTCTCCAT	1154
Db	1410	CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCAGCCATGAGCTACGTCTCCAT	1469
Qy	1155	TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCTTGGTT	1214
Db	1470	TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGCCCCATTCTTGGTT	1529
Qy	1215	CATCGTGGCCGAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT	1274
Db	1530	CATCGTGGCCGAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT	1589
Qy	1275	CTCCAAGTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT	1334
Db	1590	CTCCAAGTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT	1649
Qy	1335	GGGGCCCTACGCTTCTCTCTATTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT	1394
Db	1650	GGGGCCCTACGCTTCTCTCTATTGCGGTCCTCCTGCTGGGCTTCTTCATCTTCACCTT	1709
Qy	1395	CTTAAGAGTACCTGAAACTCGAGGCCGACGTTTGACCAGATCTCAGCTGCCTTCCACCG	1454
Db	1710	CTTAAGAGTACCTGAAACTCGAGGCCGACGTTTGACCAGATCTCGGCTGCCTTCCACCG	1769
Qy	1455	GACACCCTCTCTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC	1514



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|||||
Db      1770 GACACCCTCTCTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTTGAGTATTTAGGGCC 1829
Qy      1515 AGATGAGAACGAC 1527
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Db      1830 AGATGAGAATGAC 1842
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RESULT 14  
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 AC ABL41106;  
 XX  
 DT 12-AUG-2002 (first entry)  
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 DE Modified GLUT4 encoding nucleotide sequence.  
 XX  
 KW Protein translocation; plasma membrane; GLUT-4; diabetes mellitus;  
 KW insulin; gene; GFP; green fluorescent protein; ds.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2592  
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 FT /product= "modified GLUT4"  
 FT /note= "contains myc epitope tags and GFP"  
 FT misc\_feature 1873..2592  
 FT /\*tag= b  
 FT /note= "GFP"  
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 PN US2002052012-A1.  
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 PD 02-MAY-2002.  
 XX  
 PF 28-JUN-2001; 2001US-00894927.  
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 PR 22-MAY-1997; 97US-0047433P.  
 PR 09-JUN-1999; 99US-0138237P.  
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 PR 09-JUN-2000; 2000US-00591025.  
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 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Bogan JS, Lodish HF;  
 XX  
 DR WPI; 2002-443696/47.  
 DR P-PSDB; ABB07975.  
 XX  
 PT Determining protein translocation to the plasma membrane of a mammalian  
 PT cell using a modified protein with an intracellular fluorescent tag and  
 PT an extracellular group tag, useful in finding new drugs, particularly to  
 PT treat diabetes.  
 XX  
 PS Example 1; Fig 8a-b; 34pp; English.  
 XX  
 CC The invention relates to determining if a protein translocates from an  
 CC intracellular location to the plasma membrane of a mammalian cell in the  
 CC presence of a condition or stimulus. The method involves modifying the  
 CC protein with a group tag in the extracellular domain and a fluorescent  
 CC tag in the intracellular domain and determining the proportion of total  
 CC protein which is at the membrane. The method is used to identify a drug  
 CC which enhances translocation of a protein from an intracellular location  
 CC to the plasma membrane of a mammalian cell. The method is particularly  
 CC used to measure GLUT-4 protein translocation to identify drugs to treat  
 CC insulin resistance in adult-onset diabetes mellitus. The invention  
 CC provides a less labour intensive quantitative method for measuring GLUT4  
 CC translocation than prior art methods. The present sequence represents a  
 CC modified GLUT4 nucleotide sequence, containing myc epitope tags and green  
 CC fluorescent protein (GFP) sequences  
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 Best Local Similarity 99.6%; Pred. No. 3.2e-314;  
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 Db 510 GCTTAAGGGACCCAGCTCCATCCCTCCAGGCACCCTCACCACCCTCTGGGCCCTCTCCGT 569  
 Qy 255 GGCCATCTTTTCCGTGGGCGGCATGATTTCTCCTCCTCATTGGTATCATCTCTCAGTG 314  
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 Db 570 GGCCATCTTTTCCGTGGGCGGCATGATTTCTCCTCCTCATTGGTATCATCTCTCAGTG 629  
 Qy 315 GCTTGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 374  
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 Db 630 GCTTGAAGGAAAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTGCTGGGGGGCAGCCT 689

Low score

Qy	375	CATGGGCCTGGCCAACGCTGCTGCCTCCTATGAAATGCTCATCCTTGGACGATTCTCAT	434
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Qy	435	TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC	494
Db	750	TGGCGCCTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCC	809
Qy	495	CACTCACCTGCGGGGCGCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT	554
Db	810	CACTCACCTGCGGGGCGCCTGGGGACGCTCAACCAACTGGCCATTGTTATCGGCATTCT	869
Qy	555	GATCGCCAGGTGCTGGGCTTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCT	614
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Qy	615	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGTGCCCTTCTGTCCCGA	674
Db	930	CCTGGGCCTCACAGTGCTACCTGCCCTCCTGCAGCTGGTCTGTGCCCTTCTGTCCCGA	989
Qy	675	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	734
Db	990	GAGCCCCGCTACCTCTACATCATCCAGAATCTCGAGGGGCTGCCAGAAAGAGTCTGAA	1049
Qy	735	GCGCCTGACAGGTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	794
Db	1050	GCGCCTGACAGGTGGGCCGATGTTTCTGGAGTGCTGGCTGAGCTGAAGGATGAGAAGCG	1109
Qy	795	GAAGCTGGAGCGTGAGCGGCCACTGTCCCTGCTCCAGCTCCTGGGCAGCCGTACCCACCG	854
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Qy	855	GCAGCCCCTGATCATTGCGGTCTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	914
Db	1170	GCAGCCCCTGATCATTGCGGTCTGCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGC	1229
Qy	915	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	974
Db	1230	TGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGCCAGCCTGCCTATGC	1289
Qy	975	CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA	1034
Db	1290	CACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCGGTGTTGTTGGTGGA	1349
Qy	1035	GCGGGCGGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT	1094
Db	1350	GCGGGCGGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATGTGTGGCTGTGCCAT	1409
Qy	1095	CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCAGCCATGAGCTACGTCTCCAT	1154
Db	1410	CCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCAGCCATGAGCTACGTCTCCAT	1469
Qy	1155	TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGTAGATTGGCCCTGGCCCCATTCTTGTT	1214
Db	1470	TGTGGCCATCTTTGGCTTCGTGGCATTTTTTGTAGATTGGCCCTGGCCCCATTCTTGTT	1529
Qy	1215	CATCGTGGCCAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT	1274
Db	1530	CATCGTGGCCAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATGGCTGTGGCTGGTTT	1589
Qy	1275	CTCCAACCTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT	1334
Db	1590	CTCCAACCTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTATGTTGCGGAGGCTAT	1649
Qy	1335	GGGGCCCTACGTCTTCCTTCTATTTCGCGGTCTCCTGCTGGGCTCTTCATCTTCACCTT	1394
Db	1650	GGGGCCCTACGTCTTCCTTCTATTTCGCGGTCTCCTGCTGGGCTCTTCATCTTCACCTT	1709
Qy	1395	CTTAAGAGTACCTGAAACTCGAGGCCGACGTTTGACCAGATCTCAGCTGCCTTCCACCG	1454
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Qy	1515	AGATGAGAACGAC	1527
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Page 3 ⇒ blank

RESULT 8  
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 DEFINITION Sequence 16543 from Patent WO02068579.  
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 VERSION CQ730609.1 GI:42304929  
 KEYWORDS .  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
 TITLE Kits, such as nucleic acid arrays, comprising a majority of  
 human exons or transcripts, for detecting expression and other uses  
 thereof  
 JOURNAL Patent: WO 02068579-A 16543 06-SEP-2002; *→ unk priority.*  
 PE Corporation (NY) (US)  
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 Qy 121 AACATTGGGGTCATCAATGCCCTCAGAAGGTGATTGAACAGAGCTACAATGAGACGTGG 180  
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Qy	841	AGCCGTACCCACCGGCAGCCCCTGATCATTGCGGTCGTGCTGCAGCTGAGCCAGCAGCTC	900
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Qy	901	TCTGGCATCAATGCTGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGC	960
Db	1046	TCTGGCATCAATGCTGTTTTCTATTATTCGACCAGCATCTTCGAGACAGCAGGGGTAGGC	1105
Qy	961	CAGCCTGCCTATGCCACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCG	1020
Db	1106	CAGCCTGCCTATGCCACCATAGGAGCTGGTGTGGTCAACACAGTCTTCACCTTGGTCTCG	1165
Qy	1021	GTGTTGTGGTGGAGCGGGCGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATG	1080
Db	1166	GTGTTGTGGTGGAGCGGGCGGGCGCCGACGCTCCATCTCCTGGGCCTGGCGGGCATG	1225
Qy	1081	TGTGGCTGTGCCATCCTGATGACTGTGGCTCTGCTCCTGCTGGAGCGAGTTCCAGCCATG	1140
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Qy	1141	AGCTACGCTCTCCATTGTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTGGCCCTGGC	1200
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Qy	1201	CCCATTCTTGGTTATCGTGGCCGAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATG	1260
Db	1346	CCCATTCTTGGTTATCGTGGCCGAGCTCTTCAGCCAGGACCCCGCCGGCAGCCATG	1405
Qy	1261	GCTGTGGCTGGTTTCTCCAAGTGGACGAGCAACTTCATCATTGGCATGGGTTTCCAGTAT	1320
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Qy	1321	GTTGCGGAGGCTATGGGGCCCTACGCTTCTCTTCTATTTGCGGTCTCCTGCTGGGCTTC	1380
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Qy	1381	TTCATCTTCACCTTCTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCA	1440
Db	1526	TTCATCTTCACCTTCTTAAGAGTACCTGAAACTCGAGGCCGGACGTTTGACCAGATCTCA	1585
Qy	1441	GCTGCCTTCCACCGGACACCCTCTCTTTAGAGCAGGAGGTGAAACCCAGCACAGAACTT	1500
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Qy	1501	GAGTATTTAGGGCCAGATGAGAACGACTGA	1530
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